
GCCCCACCACGCCTCATCTGTGACAGCCGAGTCCTGGAGAGGTACCTCTTGGAGGCCAAG
1 60
CGGGGTGGTGCGGAGTAGACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTTC
AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys
GAGGCCGAGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACT
61 120
CTCCGGCTCTTATAGTGCTGCCCGACACGACTTGTGACGTCGAACTTACTCTTATAGTGA
GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr
GTCCCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGGATGGAGGTCGGGCAGCAGGCC
121 180
CAGGGTCTGTGGTTTCAATTAAAGATACGGACCTTCTCCTACCTCCAGCCCGTCGTCCGG
ValProAspThrLysValAsnPheTyrAlaTrpLysArgMetGluValGlyGlnGlnAla
GTAGAAGTCTGGCAGGGCCTGGCCCTGCTGTCGGAAGCTGTCCTGCGGGGCCAGGCCCTG
181 240
CATCTTCAGACCGTCCCGGACCGGGACGACAGCCTTCGACAGGACGCCCCGGTCCGGGAC
ValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu
TTGGTCAACTCTTCCCAGCCGTGGGAGCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGT
241 300
AACCAGTTGAGAAGGGTCGGCACCCTCGGGGACGTCGACGTACACCTATTTCGGCAGTCA
LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer
GGCCTTCGCAGCCTCACCACTCTGCTTCGGGCTCTGGGAGCCCAGAAGGAAGCCATCTCC
301 360
CCGGAAGCGTCGGAGTGGTGAGACGAAGCCCGAGACCCTCGGGTCTTCCTTCGGTAGAGG
GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer
CCTCCAGATGCGGCCTCAGCTGCTCCACTCCGAACAATCACTGCTGACACTTTCCGCAAA
361 420
GGAGGTCTACGCCGGAGTCGACGAGGTGAGGCTTGTTAGTGACGACTGTGAAAGGCGTTT
ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys
CTCTTCCGAGTCTACTCCAATTTCCTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCC
421 480
GAGAAGGCTCAGATGAGGTTAAAGGAGGCCCCTTTCGACTTCGACATGTGTCCCCTCCGG
LeuPheArgValTyrSerAsnPheLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla
TGCAGGACAGGGGACAGATGA (SEQ ID NO:120)
481 501
ACGTCCTGTCCCCTGTCTACT (SEQ ID NO:135)
CysArgThrGlyAspArg (SEQ ID NO:121)

Figure 5